#3

SEQUENCE LISTING

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ANDERSON, KIM V.
BORNAES, CLAUS

<120> FACTOR VII OR VIIA-LIKE MOLECULES

<130> 31-001100US

<140> 09/782,587
<141> 2001-02-12

<150> PA 2000 00218
<151> 2000-02-11

<150> 60/184,036
<151> 2000-02-22

<150> 60/241,916
<151> 2000-10-18

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<170> PatentIn Ver. 2.1

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             20                  25                  30

Asp Ala Xaa Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp
         35                  40                  45

Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln
     50                  55                  60

Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn
 65                  70                  75                  80

Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly
                 85                  90                  95

Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys
            100                 105                 110

Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr
        115                 120                 125

Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg
    130                 135                 140

Asn Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro
145                 150                 155                 160

Lys Gly Glu Cys Pro Trp Gln Val Leu Leu Leu Val Asn Gly Ala Gln
                165                 170                 175

Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala
            180                 185                 190

His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu
        195                 200                 205

Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg
    210                 215                 220

Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn
225                 230                 235                 240

His Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp
                245                 250                 255

His Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr
            260                 265                 270

Leu Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu
        275                 280                 285
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Asp Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg
    290                 295                 300

Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser
305                 310                 315                 320

Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser
                325                 330                 335

Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr
            340                 345                 350

Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys
        355                 360                 365

Ala Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile
    370                 375                 380

Glu Trp Leu Gln Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu
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Leu Arg Ala Pro Phe Pro
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gccgtcttcg tcacccagga ggaagcccat ggcgtcctgc atcgccggcg ccgg gcc   117
                                                            Ala
                                                             1

aat gcc ttt ctg gaa gag ctc cgc cct ggc tcc ctg gaa cgc gaa tgc   165
Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu Cys
              5                  10                  15

aaa gag gaa cag tgc agc ttt gag gaa gcc cgg gag att ttc aaa gac   213
Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys Asp
         20                  25                  30

gct gag cgg acc aaa ctg ttt tgg att agc tat agc gat ggc gat cag   261
Ala Glu Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln
     35                  40                  45

tgc gcc tcc agc cct tgc cag aac ggg ggc tcc tgc aaa gac cag ctg   309
Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln Leu
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cag agc tat atc tgc ttc tgc ctg cct gcc ttt gag ggg cgc aat tgc   357
Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn Cys
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gaa acc cat aag gat gac cag ctg att tgc gtc aac gaa aac ggg ggc   405
Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly Gly
             85                  90                  95

tgc gag cag tac tgc agc gat cac acg ggc acg aag cgg agc tgc cgc   453
Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys Arg
        100                 105                 110

tgc cac gaa ggc tat agc ctc ctg gct gac ggg gtg tcc tgc acg ccc   501
Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr Pro
    115                 120                 125

acg gtg gaa tac cct tgc ggg aag att ccc att cta gaa aag cgg aac   549
Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg Asn
130                 135                 140                 145

gct agc aaa ccc cag ggc cgg atc gtc ggc ggg aag gtc tgc cct aag   597
Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro Lys
                150                 155                 160

ggg gag tgc ccc tgg cag gtc ctg ctc ctg gtc aac ggg gcc cag ctg   645
Gly Glu Cys Pro Trp Gln Val Leu Leu Leu Val Asn Gly Ala Gln Leu
            165                 170                 175

tgc ggc ggg acc ctc atc aat acc att tgg gtc gtg tcc gcc gct cac   693
Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala His
        180                 185                 190

tgc ttc gat aag att aag aat tgg cgg aac ctc atc gct gtg ctc ggc   741
Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu Gly
    195                 200                 205

gaa cac gat ctg tcc gag cat gac ggg gac gaa cag tcc cgc cgg gtg   789
Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg Val
210                 215                 220                 225

gct cag gtc atc att ccc tcc acc tat gtg cct ggc acg acc aat cac   837
Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn His
                230                 235                 240

gat atc gct ctg ctc cgc ctc cac cag ccc gtc gtg ctc acc gat cac   885
Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp His
            245                 250                 255

gtc gtg cct ctg tgc ctg cct gag cgg acc ttt agc gaa cgc acg ctg   933
Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr Leu
        260                 265                 270

gct ttc gtc cgc ttt agc ctc gtg tcc ggc tgg ggc cag ctg ctc gac   981
Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu Asp
    275                 280                 285
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cgg ggc gct acc gct ctc gag ctg atg gtg ctc aac gtc ccc cgg ctg   1029
Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg Leu
290                 295                 300                 305

atg acc cag gac tgc ctg cag cag tcc cgc aaa gtg ggg gac tcc ccc   1077
Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser Pro
                310                 315                 320

aat atc acg gag tat atg ttt tgc gct ggc tat agc gat ggc tcc aag   1125
Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser Lys
            325                 330                 335

gat agc tgc aag ggg gac tcc ggc ggg ccc cat gcc acg cac tat cgc   1173
Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr Arg
        340                 345                 350

ggg acc tgg tac ctc acc ggg atc gtc agc tgg ggc cag ggc tgc gcc   1221
Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys Ala
    355                 360                 365

acg gtg ggg cac ttt ggc gtc tac acg cgc gtc agc cag tac att gag   1269
Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile Glu
370                 375                 380                 385

tgg ctg cag aag ctc atg cgg agc gaa ccc cgg ccc ggg gtg ctc ctg   1317
Trp Leu Gln Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu Leu
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Arg Ala Pro Phe Pro
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<210> 3
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<213> Homo sapiens

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Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys
             20                  25                  30

Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp
         35                  40                  45

Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln
     50                  55                  60

Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn
 65                  70                  75                  80

Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly
                 85                  90                  95
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Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys
            100                 105                 110

Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr
        115                 120                 125

Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg
    130                 135                 140

Asn Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro
145                 150                 155                 160

Lys Gly Glu Cys Pro Trp Gln Val Leu Leu Leu Val Asn Gly Ala Gln
                165                 170                 175

Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala
            180                 185                 190

His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu
        195                 200                 205

Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg
    210                 215                 220

Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn
225                 230                 235                 240

His Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp
                245                 250                 255

His Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr
            260                 265                 270

Leu Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu
        275                 280                 285

Asp Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg
    290                 295                 300

Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser
305                 310                 315                 320

Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser
                325                 330                 335

Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr
            340                 345                 350

Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys
        355                 360                 365

Ala Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile
    370                 375                 380

Glu Trp Leu Gln Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu
385                 390                 395                 400
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Leu Arg Ala Pro Phe Pro
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<212> DNA
<213> Artificial Sequence

<220>
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gcgccgggcc aatgcctttc tggaagagct ccgccctggc tccctggaac gcgaatgcaa 180
agaggaacag tgcagctttg aggaagcccg ggagattttc aaagacgctg agcggaccaa 240
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tcccattcta gaaaagcgga acgctagcaa accccagggc cggatcgtcg gcgggaaggt 600
ctgccctaag ggggagtgcc cctggcaggt cctgctcctg gtcaacgggg cccagctgtg 660
cggcgggacc ctcatcaata ccatttgggt cgtgtccgcc gctcactgct tcgataagat 720
taagaattgg cggaacctca tcgctgtgct cggcgaacac gatctgtccg agcatgacgg 780
ggacgaacag tcccgccggg tggctcaggt catcattccc tccacctatg tgcctggcac 840
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caccgggatc gtcagctggg gccagggctg cgccacggtg gggcactttg gcgtctacac 1260
gcgcgtcagc cagtacattg agtggctgca gaagctcatg cggagcgaac cccggcccgg 1320
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<210> 5
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<212> DNA
<213> Artificial Sequence

<220>
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<210> 6
<211> 31
<212> DNA
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<400> 6
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<210> 7
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer CBProFpr216

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cttaaggatc ccgccaccat ggtcagccag 30

<210> 8
<211> 28
<212> DNA
<213> Artificial Sequence

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<400> 8
ggagtccccg gttttgttgg actgctgc 28

<210> 9
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<210> 10
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<220>
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<400> 10
gcagcagtcc aacaaaaccg gggactcc 28

<210> 11
<211> 30
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<213> Artificial Sequence

<220>
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cattctagaa aaccggaccg ctagcaaacc 30

<210> 12
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<400> 12
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<210> 13
<211> 8
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<220>
<223> Description of Artificial Sequence: synthetic peptide tag

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<210> 14
<211> 10
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<220>
<223> Description of Artificial Sequence: synthetic peptide tag

<400> 14
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<210> 15
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<212> PRT
<213> Artificial Sequence

<220>
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<210> 16
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<213> Artificial Sequence

<220>
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<210> 17
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
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<400> 17
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<210> 18
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide tag

<400> 18
Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 19
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide tag

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